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TRFP CHAIN 1, LEADER A

10	20	30	40	50	60
CTGCATCATGAAGGGGGCTCGTGTTCCTCGTGCTTCTCTGGGCTGCCTTGCTCTTGATCTG					
C I M K G A R V L V L L W A A L L L I W					
<hr/>					
70	80	90	100	110	120
GGGTGGAAATTGTGAAATTTGCCAGCCGTGAAGAGGGATGTTGACCTATTCCTGACGGG					
G G N C E I C P A V K R D V D L F L T G					
<hr/>					
130	140	150	160	170	180
AACCCCCGACGPATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGTATTGGA					
T P D E Y V E Q V A Q Y K A L P V V L E					
<hr/>					
190	200	210	220	230	240
AAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAAGGAGAA					
N A R I L K N C V D A K M T E E D K E N					
<hr/>					
250	260	270	280	290	300
TGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCATCACTG					
A L S L L D K I Y T S P L C -					
<hr/>					
310	320	330	340	350	360
CCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTGCCATGT					
<hr/>					
370	380	390	400	410	
CCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTGGCAATTCAAACAAAAAAA					

Fig. 1



TRFP CHAIN 1, LEADER B

10 20 30 40 50 60
GGCCTGGCGGTGCTCCTGGAAAAGGATGTTAGACGCAGCCCTCCCACCCTGCCCTACTGT
A W R C S W K R M L D A A L P P C P T V

70 80 90 100 110 120
TGCGGCCACAGCAGATTGTGAAATTGCCCAGCCGTGAAGAGGGATGTTGACCTATTCTT
A A T A D C E I C P A V K R D V D L F L

130 140 150 160 170 180
GACGGGAACCCCGACGAATATGTTGAGCAAGTGGCACAATACAAAGCACTACCTGTAGT
T G T P D E Y V E Q V A Q Y K A L P V V

190 200 210 220 230 240
ATTGGAATGCCAGAATACTGAAGAACTGCGTTGATGCAAAAATGACAGAAGAGGATAA
L E N A R I L K N C V D A K M T E E D K

250 260 270 280 290 300
GGAGAATGCTCTCAGCTTGCTGGACAAAATATACACAAGTCCTCTGTGTTAAAGGAGCCA
E N A L S L L D K I Y T S P L C - R S H

310 320 330 340 350 360
TCACTGCCAGGAGCCCTAAGGAAGCCACTGAACTGATCACTAAGTAGTCTCAGCAGCCTG

370 380 390 400 410 420
CCATGTCCAGGTGTCTTACTAGAGGATTCCAGCAATAAAAGCCTTGCAATTCAAACAAAA

Fig. 2



TRFP CHAIN 2, LONG FORM

10	20	30	40	50	60
TGACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGT					
D T M R G A L L V L A L L V T Q A L G V					
<hr/>					
70	80	90	100	110	120
CAAGATGGCGGAAACTTGCCCCATTTTTTATGACGTCTTTTTTGCGGTGGCCAATGGAAA					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
TGAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGC					
E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
CATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGG					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
ACTAGTCATGACAACCATCAGCTCCAGCAAAGATTGCATGGGTGAAGCAGTTCAGAACAC					
L V M T T I S S S K D C M G E A V Q N T					
310	320	330	340	350	360
CGTAGAAGATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCTTC					
V E D L K L N T L G R -					
370	380	390	400	410	420
TGAGCCCCATCCTCCTGCCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCT					
430	440	450	460	470	
CACCTAATTCACTCTCAATCAGGCTGACTAGAATAAAATAACTGCATCTTAAAAAA					

Fig. 3



TRFP I CHAIN 2, SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC					
D T M R G A L L V L A L L V T Q A L G V					
<hr/>					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGC GGTGGCCAATGGAAAT					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC					
E L L L D L S L T K V N A T E P E R V A					
190	200	210	220	230	240
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGGA					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGATAGCCATCAACGAATATTGCATGGGTGAAGCAGTTCAGAACACCGTAGAA					
L V M I A I N E Y C M G E A V Q N T V E					
310	320	330	340	350	360
GATCTCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCC					
D L K L N T L G R -					
370	380	390	400	410	420
CATCCTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAA					
430	440	450	460		
TTCACTCTCAATCAGGCTGACTAGATAAAATAACTGCATCTTAAAAAA					

Fig. 4



TRFP CHAIN 2, TRUNCATED SHORT FORM

10	20	30	40	50	60
GACACGATGAGGGGGGCACTGCTTGTGCTGGCATTGCTGGTGACCCAAGCGCTGGGCGTC					
D T M R G A L L V L A L L V T O A L G V					
<hr/>					
70	80	90	100	110	120
AAGATGGCGGAGACGTGCCCCATTTTTTATGACGTCTTTTTTGCGGTGGCCAATGGAAT					
K M A E T C P I F Y D V F F A V A N G N					
130	140	150	160	170	180
GAATTACTGTTGGACTTGTCCCTCACAAAAGTCAATGCTACTGAACCAGAGAGAACAGCC					
E L L L D L S L T K V N A T E P E R T A					
190	200	210	220	230	240
ATGAAAAAATCCAGGATTGCTACGTGGAGAACGGACTCATATCCAGGGTCTTGGATGGA					
M K K I Q D C Y V E N G L I S R V L D G					
250	260	270	280	290	300
CTAGTCATGCCATCAACGAATATTGCATGGGTGAAGCAGTTTCAGAACACCGTAGAAGATC					
L V M P S T N I A W V K Q F R T P -					
310	320	330	340	350	360
TCAAGCTGAACACTTTGGGGAGATGAATCTTTGCCACTGATGCCCCTTCTGAGCCCCATC					
370	380	390	400	410	420
CTCCTGTCCTGTTCTTTACACCTAAAGCTGGAATCCAGACACCTGTCCTCACCTAATTCA					
430	440	450	460		
CTCTCAATCAGGCTGACTAGATAAAATAAAGTGCATCTTAAAAA					

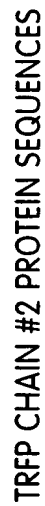
Fig. 5



TRFP CHAIN #1 PROTEIN SEQUENCE

	-20	-10	
C1 Leader A	C I M K G A R V L V L L W A A L L L I W G G N C		
C1 Leader B	A W R C S W K R M L D A A L P P C P T B A A T A D C		
	5	10	15
	20	25	30
	35		
C1	E I C P A V K R D V D L F L T G T P D E Y V E Q V A Q Y K A L P V L		
PRO.	- - - - -	- - - - -	- - - - -
	40	45	50
	55	60	65
	70		
C1	E N A R I L K N C V D A K M T E E D K E N A L S L L D K I Y T S P L C		
PRO.	- - - - -	- - - - -	- - - - -

Fig. 6



-10

C2 Leader

DTMRGALLVLLALLVTQALG

	5	10	15	20	25	30	35	40																															
C2L	V	R	M	A	E	T	C	P	I	F	Y	D	V	F	F	A	V	A	N	G	N	E	L	L	D	L	S	L	T	R	V	N	A	T	E	P	E	R	T

C2S	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
C2ST	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
PRO.	-	-	-	-	-	-	-	-	-	-	-	-	X	-	-	-	-	-	-

Fig. 7A

Fig. 7B



PATIENT # 131.2 2° (TRFP:1°)

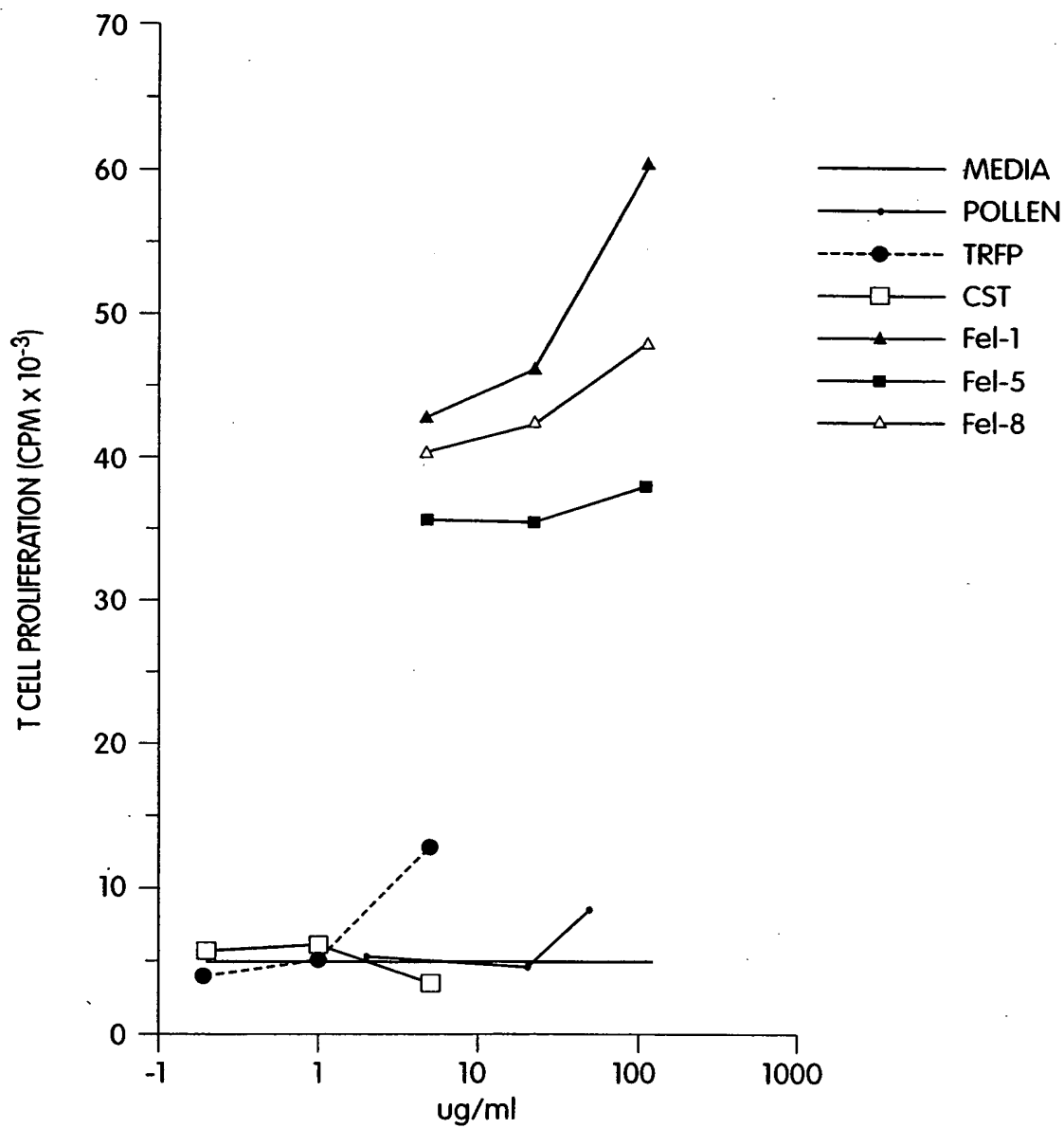


Fig. 8

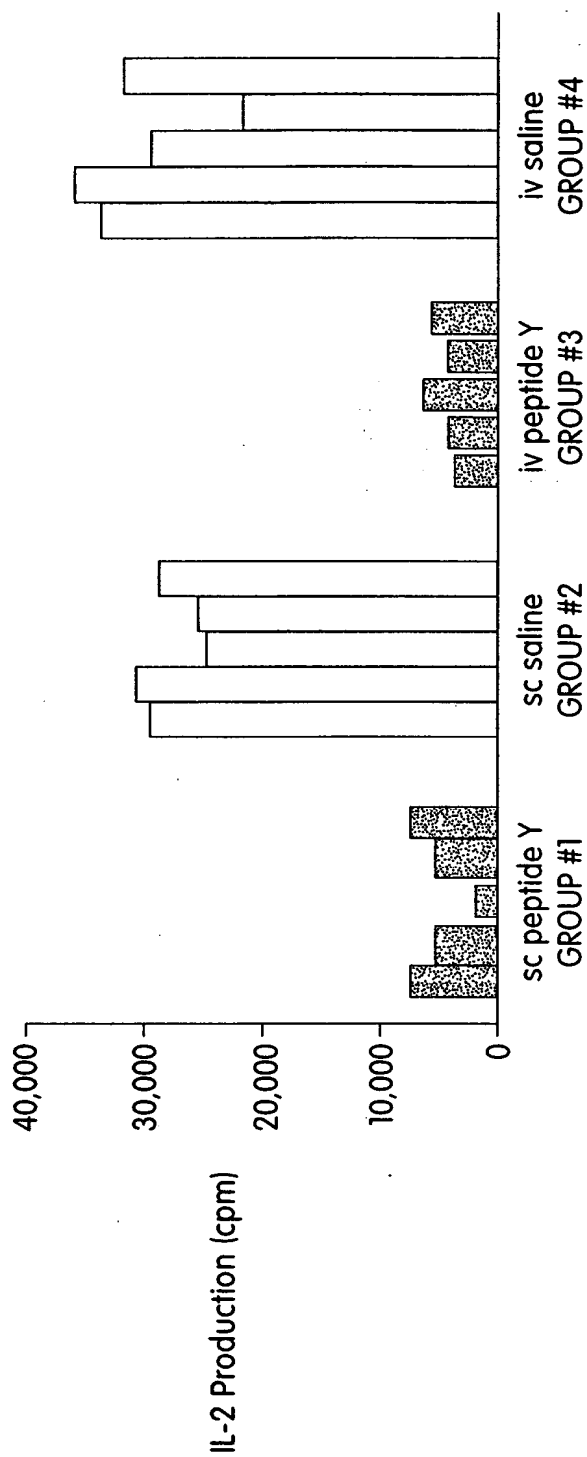
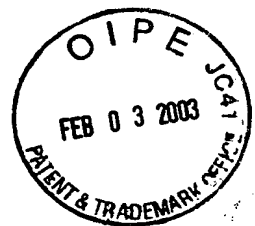


Fig. 9

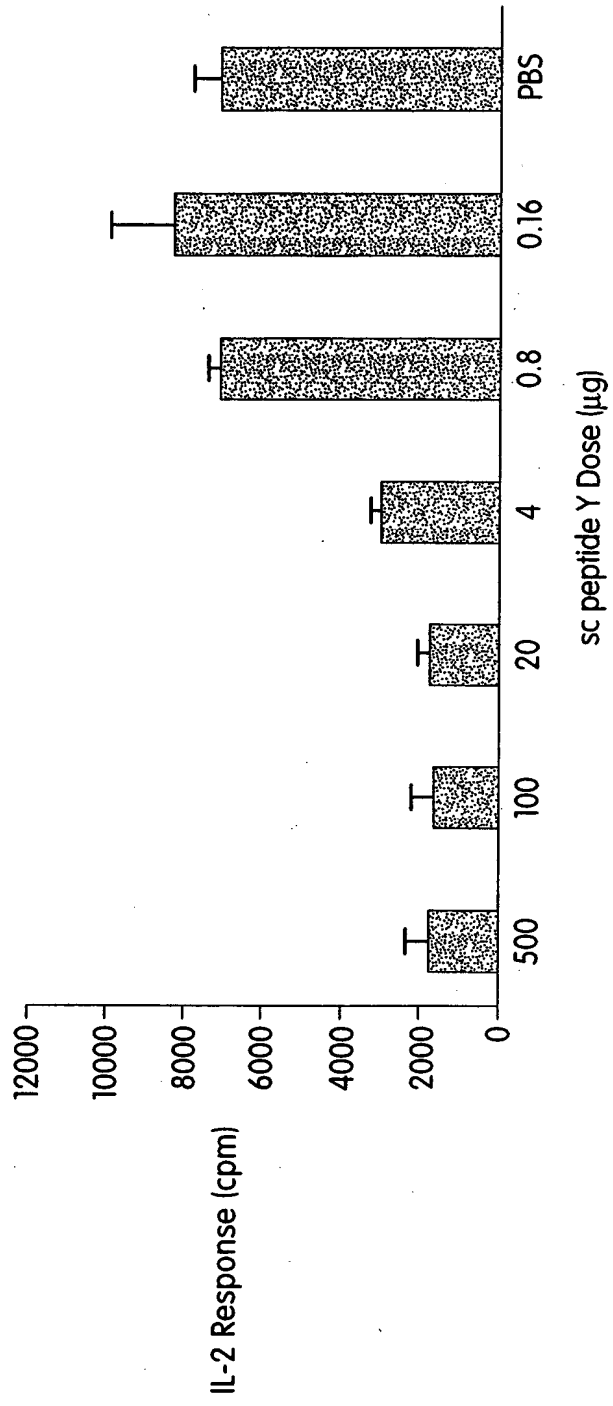


Fig.10

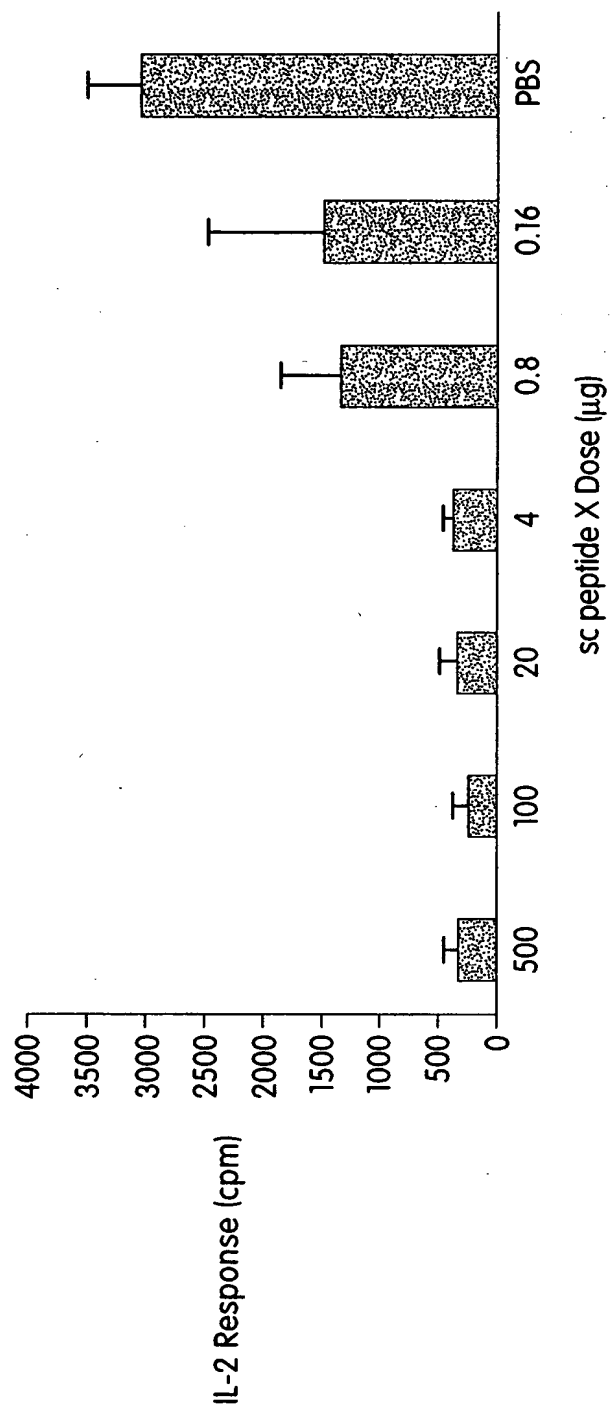
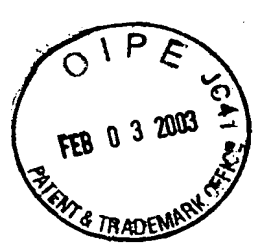


Fig.11

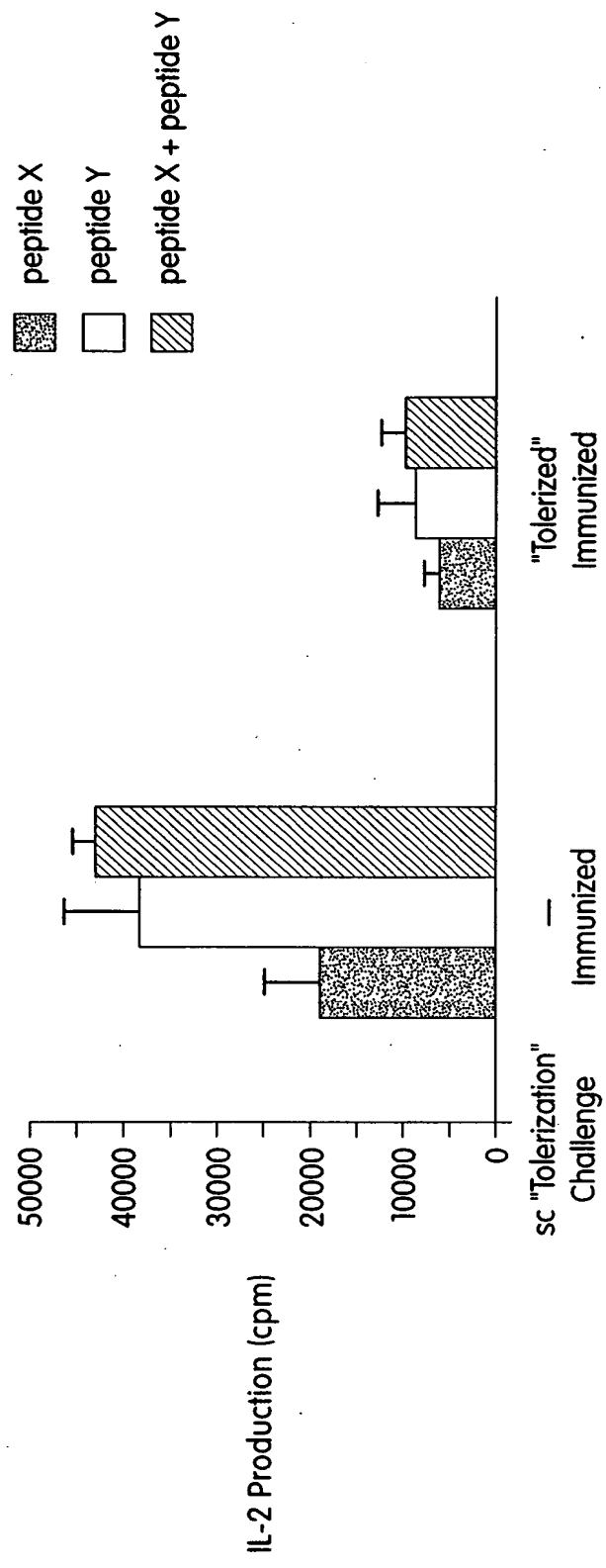


Fig.12

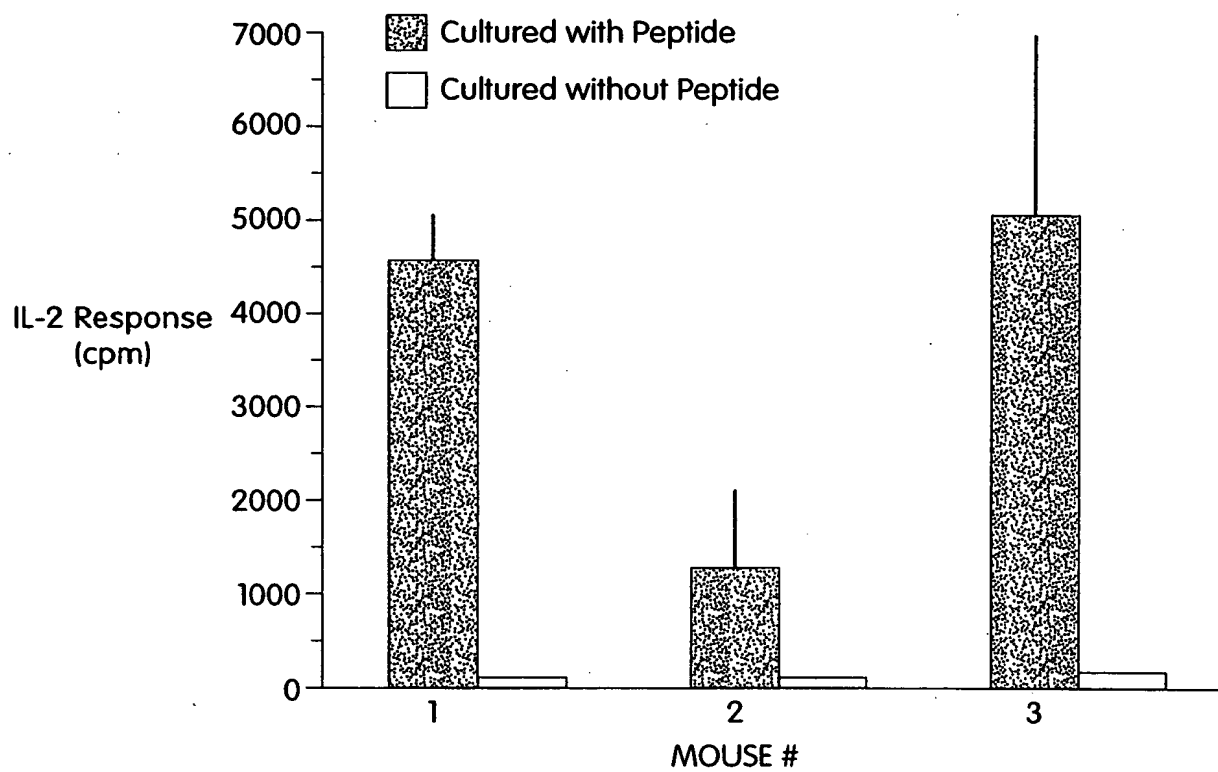


Fig. 13

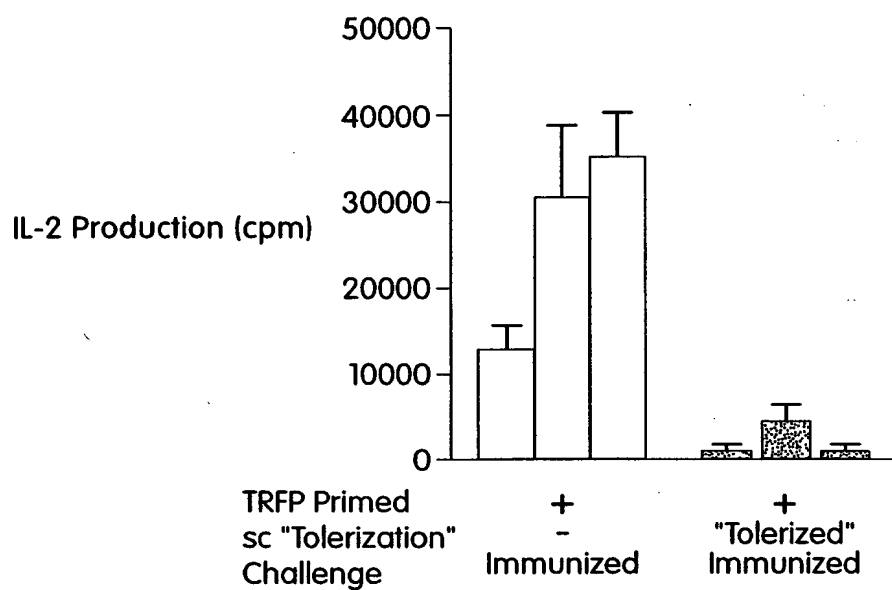


Fig. 14A

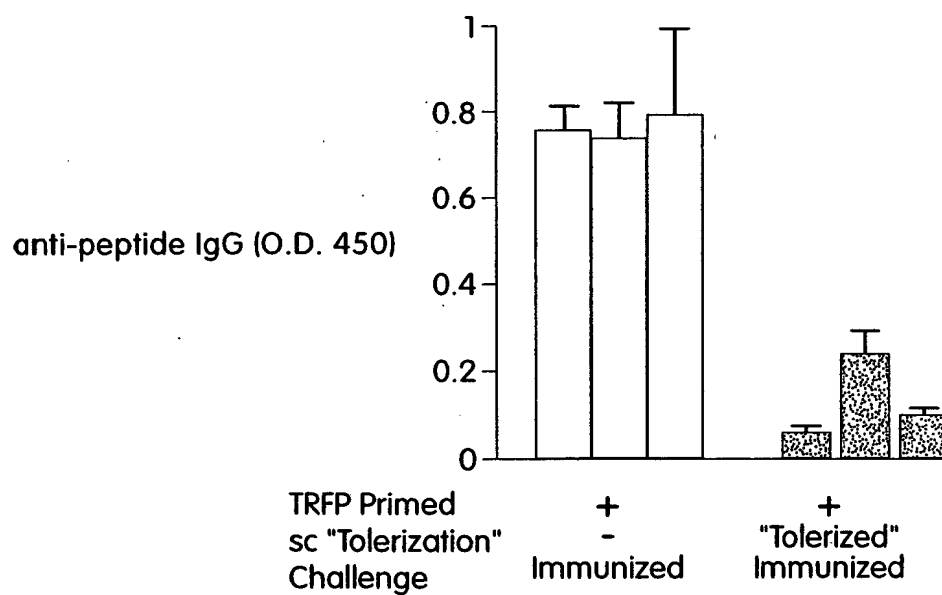


Fig. 14B

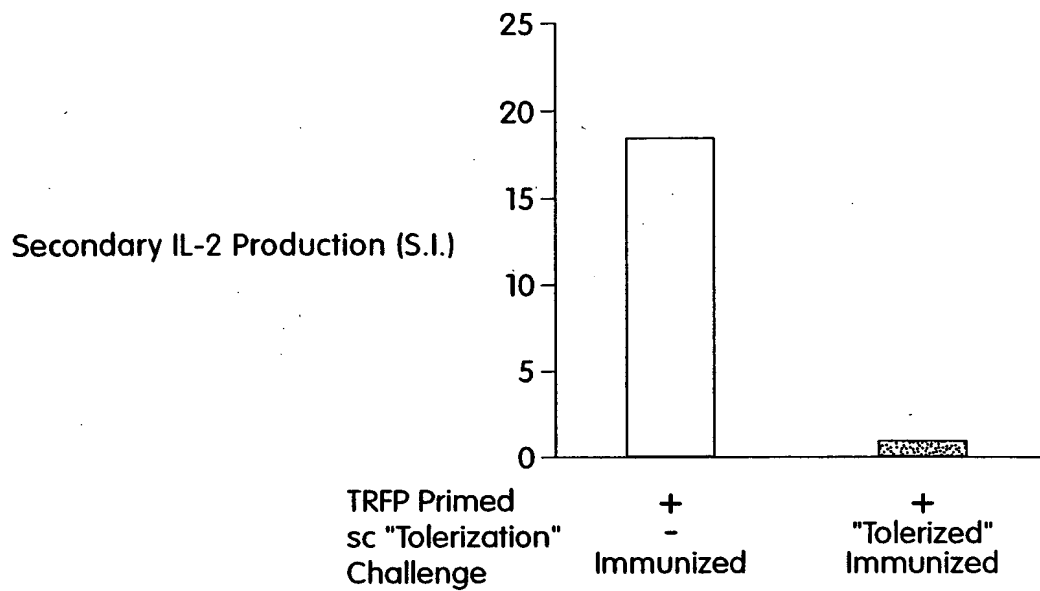


Fig. 15A

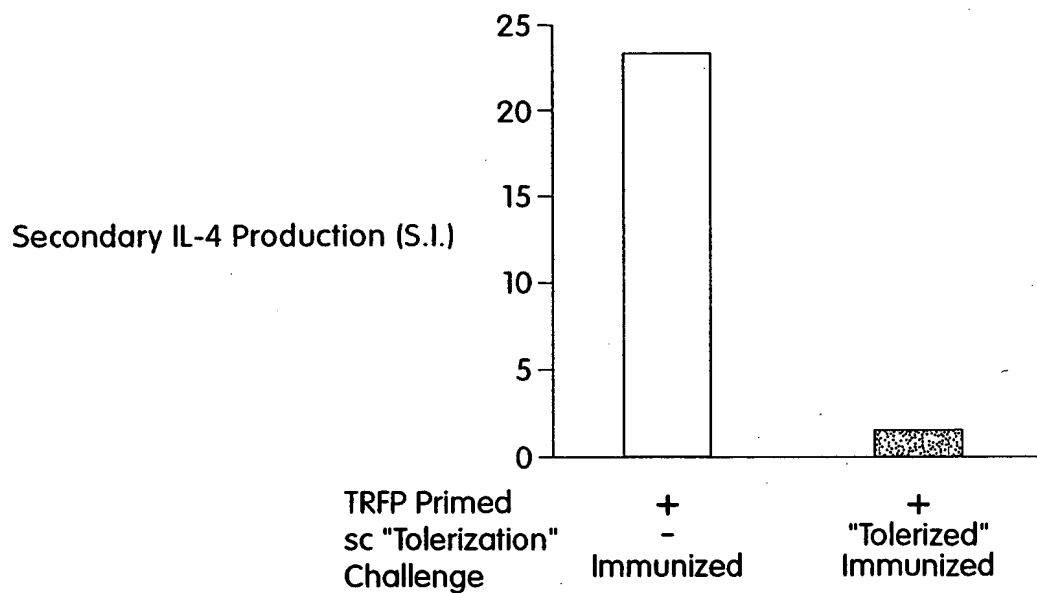


Fig. 15B

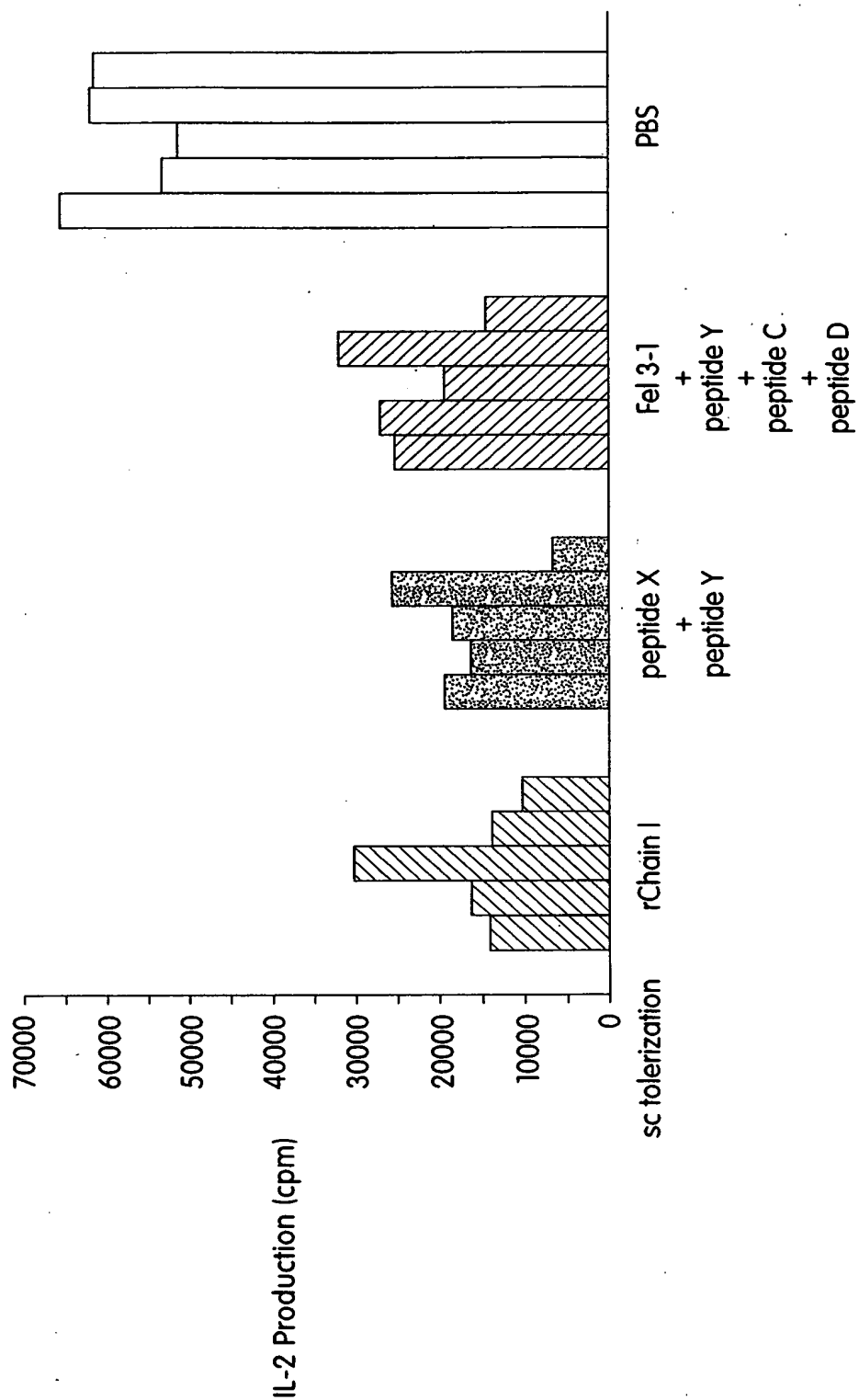


Fig. 16



SEQUENCE

PEPTIDE
NAME

X	KRDVDLFLTGTPDEYVEQVAQYKALPV
Y	KALPVVLENARILKNCVDAKMTEEDKE
Z	FFAVANGNELLLDLSLTKVNATEPER
A	EEDKENALSLLDKIYTSPL
B	MGEAVQNTVEDLKLNTLGR
C	EEDKENALSLLDKIYT
D	NALSLLDKIYTSPL

Fig. 17



Fel 32 VKMAETCPIFYDVFFAVA
Fel 33 FYDVFFAVANGNELLLD
Fel 34 NGNELLLDLSLTKVNATE
Fel 35 SLTKVNATEPERTAMKKI
Fel 36 ERTAMKKIQDCYVENGL
Fel 37 QDCYVENGLISRVLDGLV
Fel 38 ISRVLDGLVMTTISSSKDCM
Fel 38-1 ISRVLDGLVMIAINE**DCM
Fel 39 MTTISSSKDCMGEAVQNTTEVELDKLNTLGF
Fel 39.1 MIAINE**DCMGEAVQNTTEVELDKLNTLGF

Fig. 18

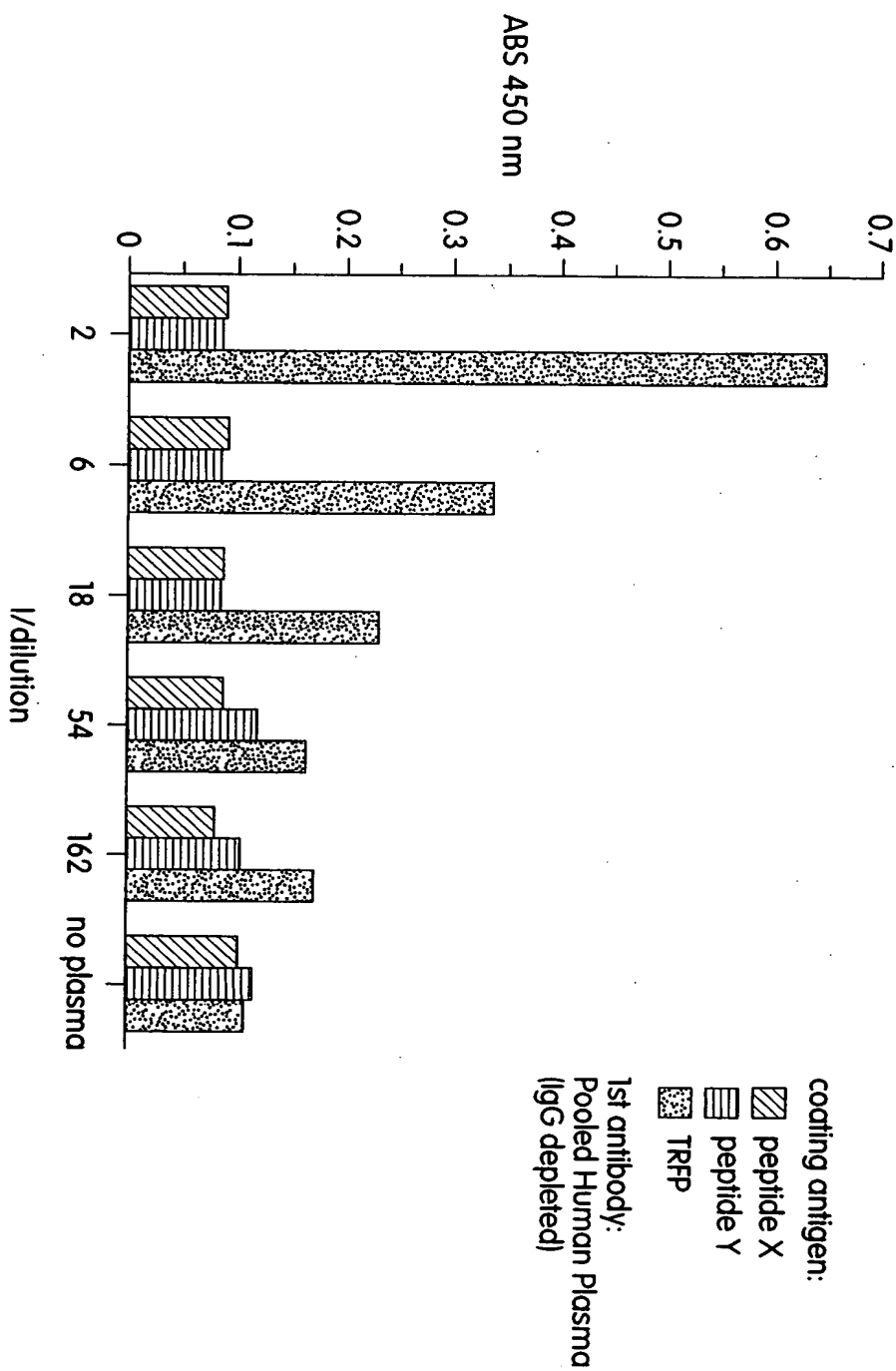


Fig. 19

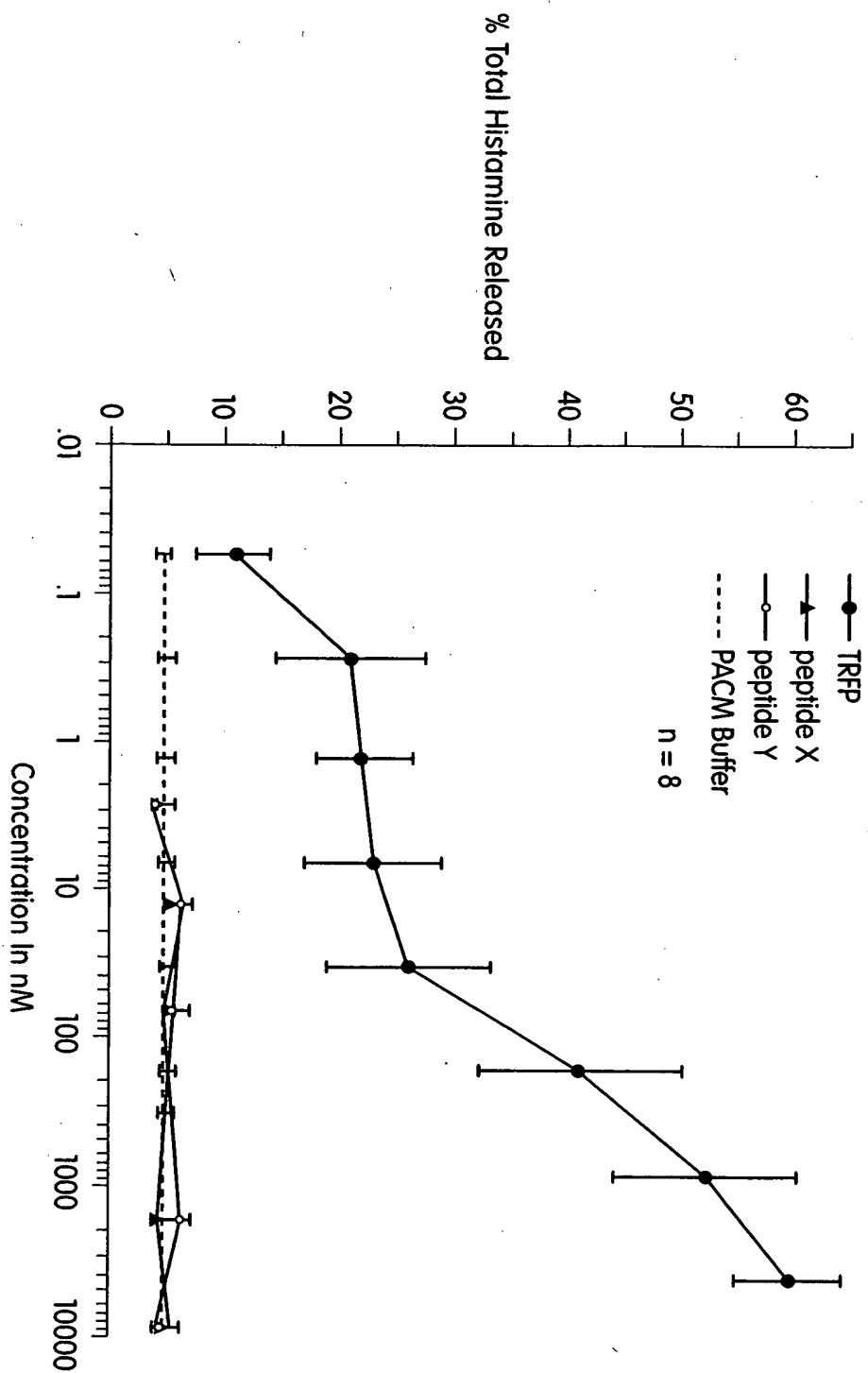


Fig. 20

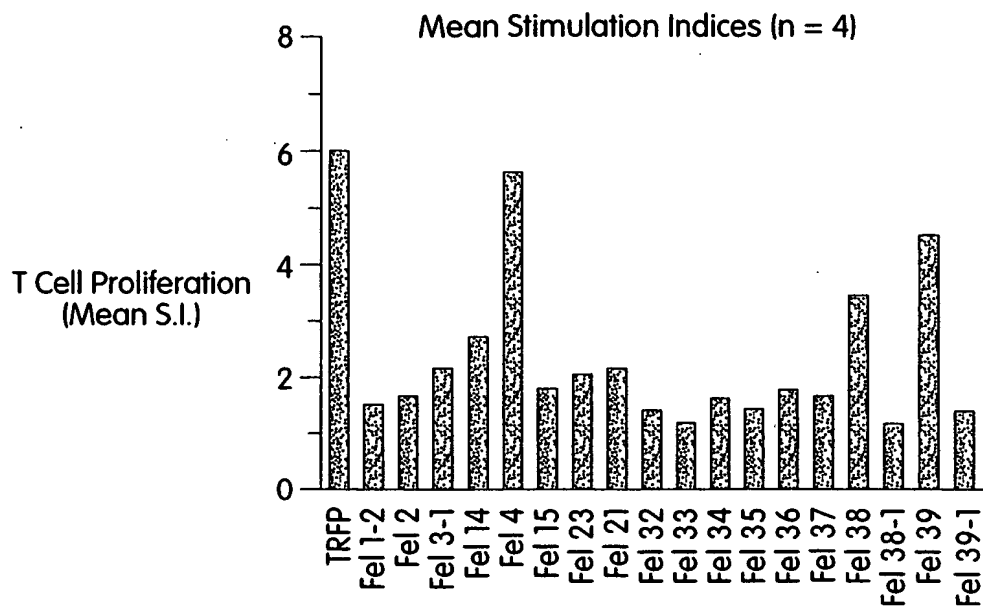


Fig. 21A

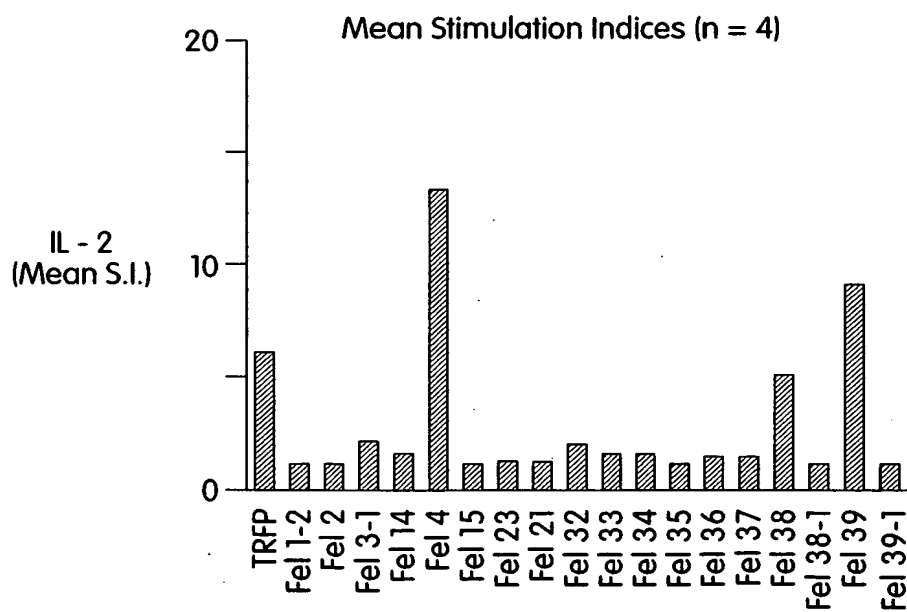


Fig. 21B

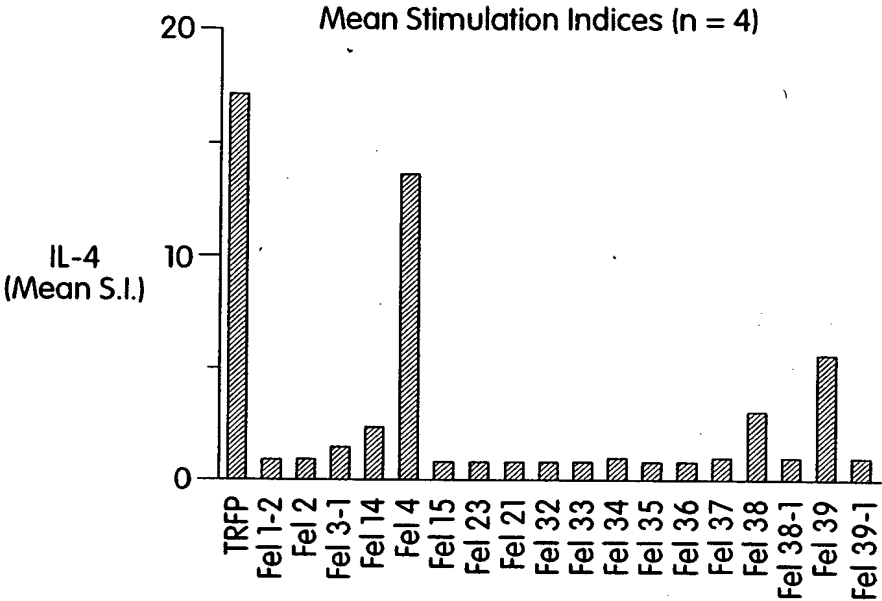


Fig. 21C

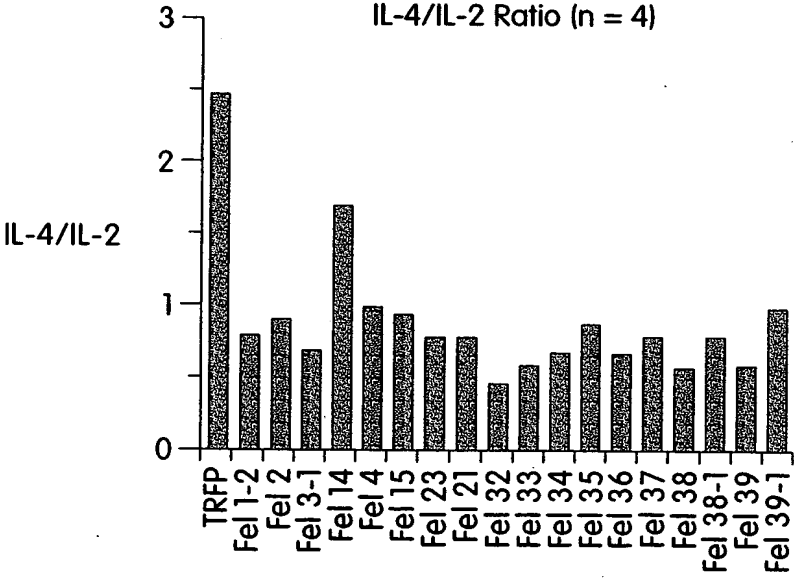
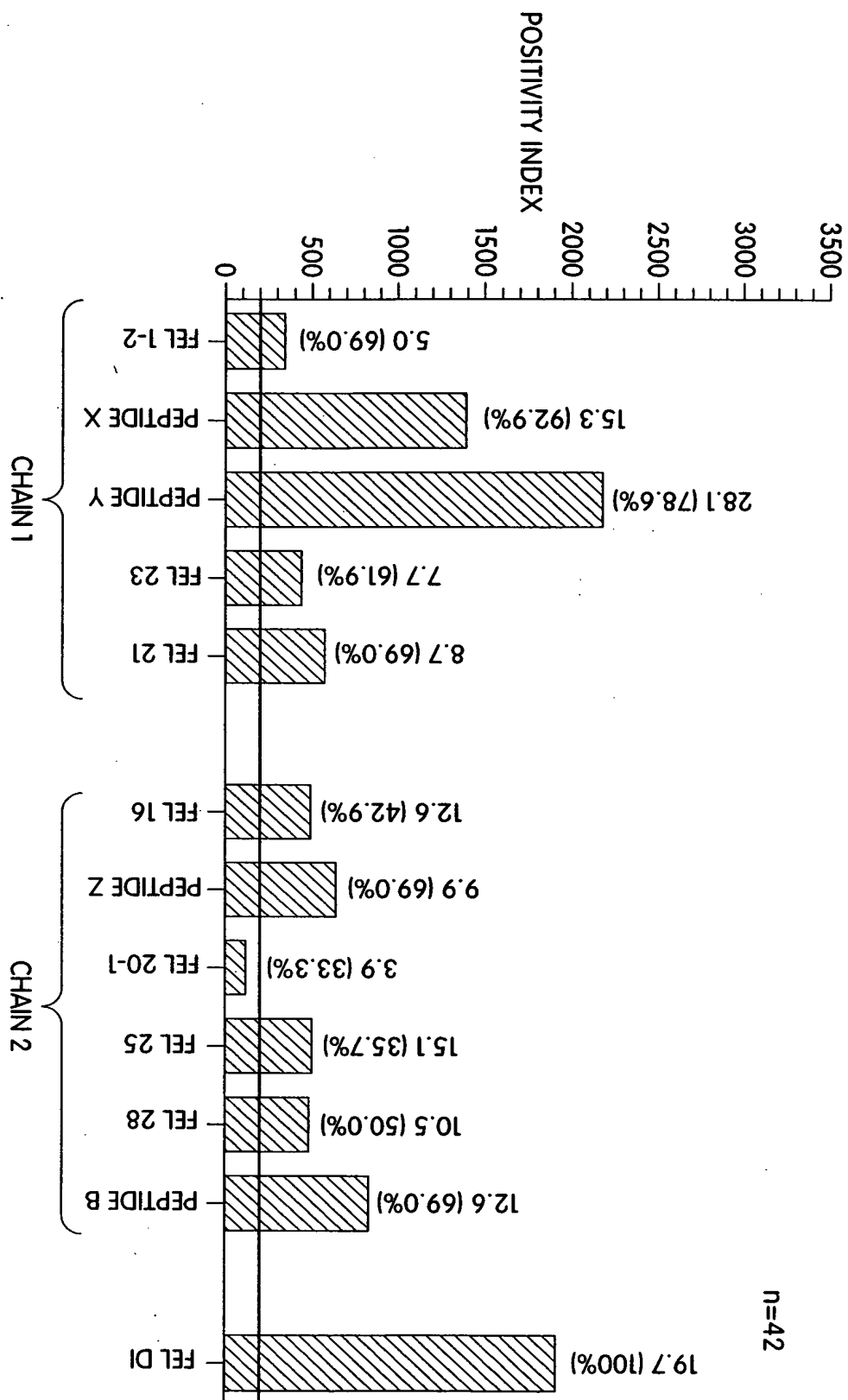


Fig. 22

Fig. 23



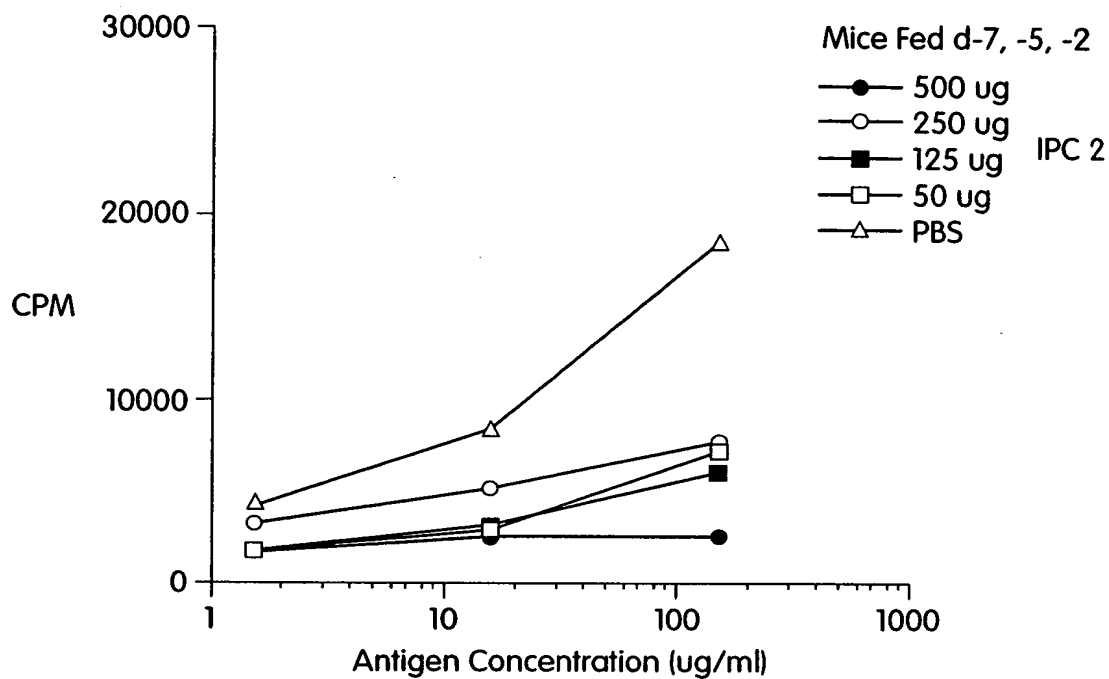


Fig. 24A

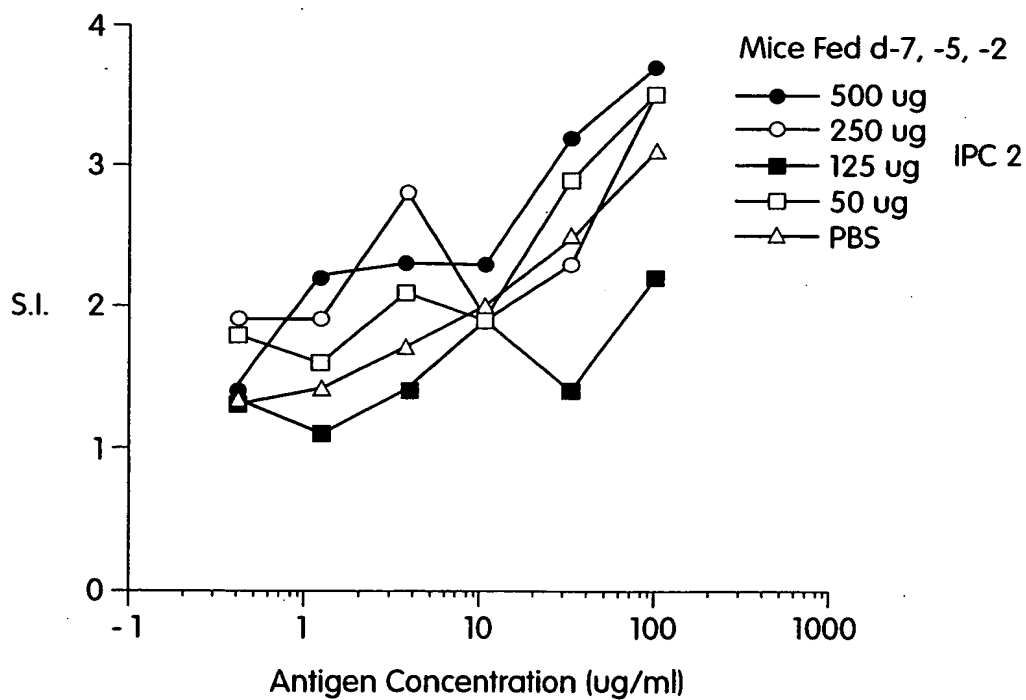


Fig. 24B

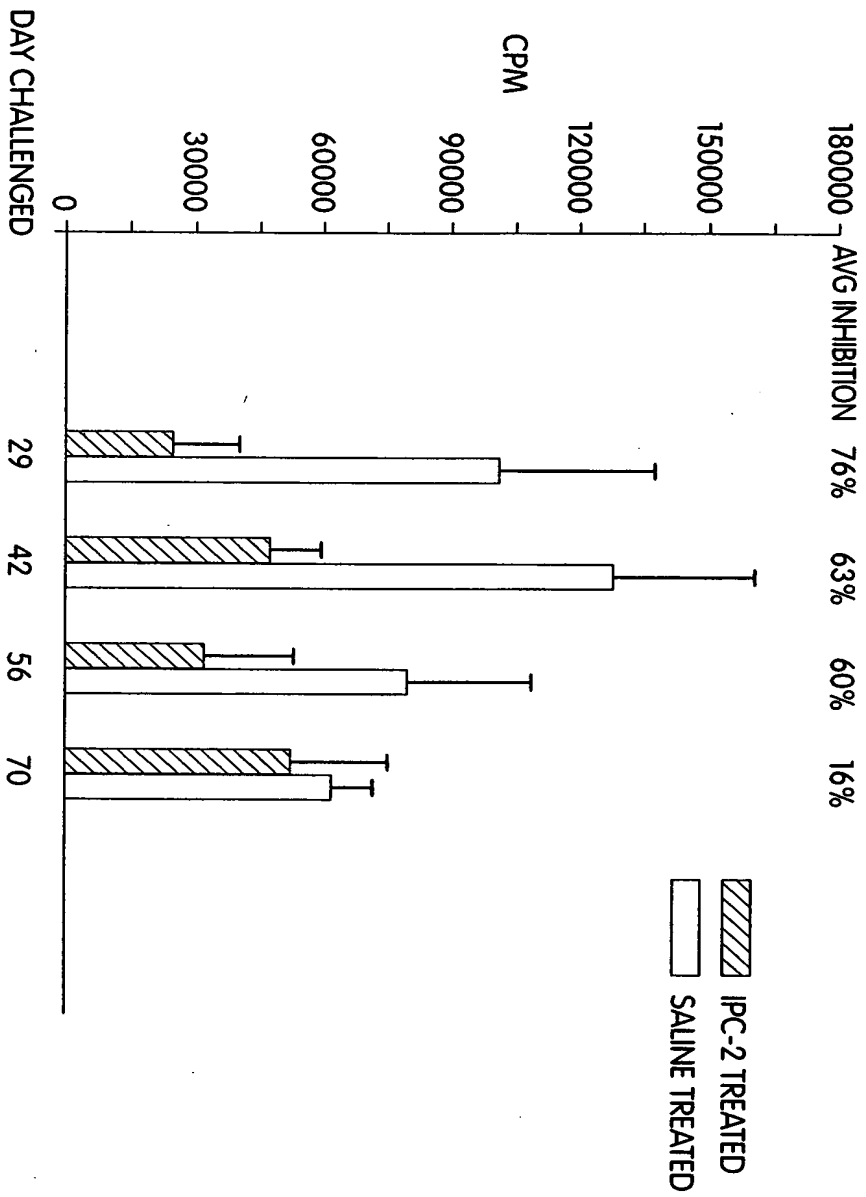


Fig. 25

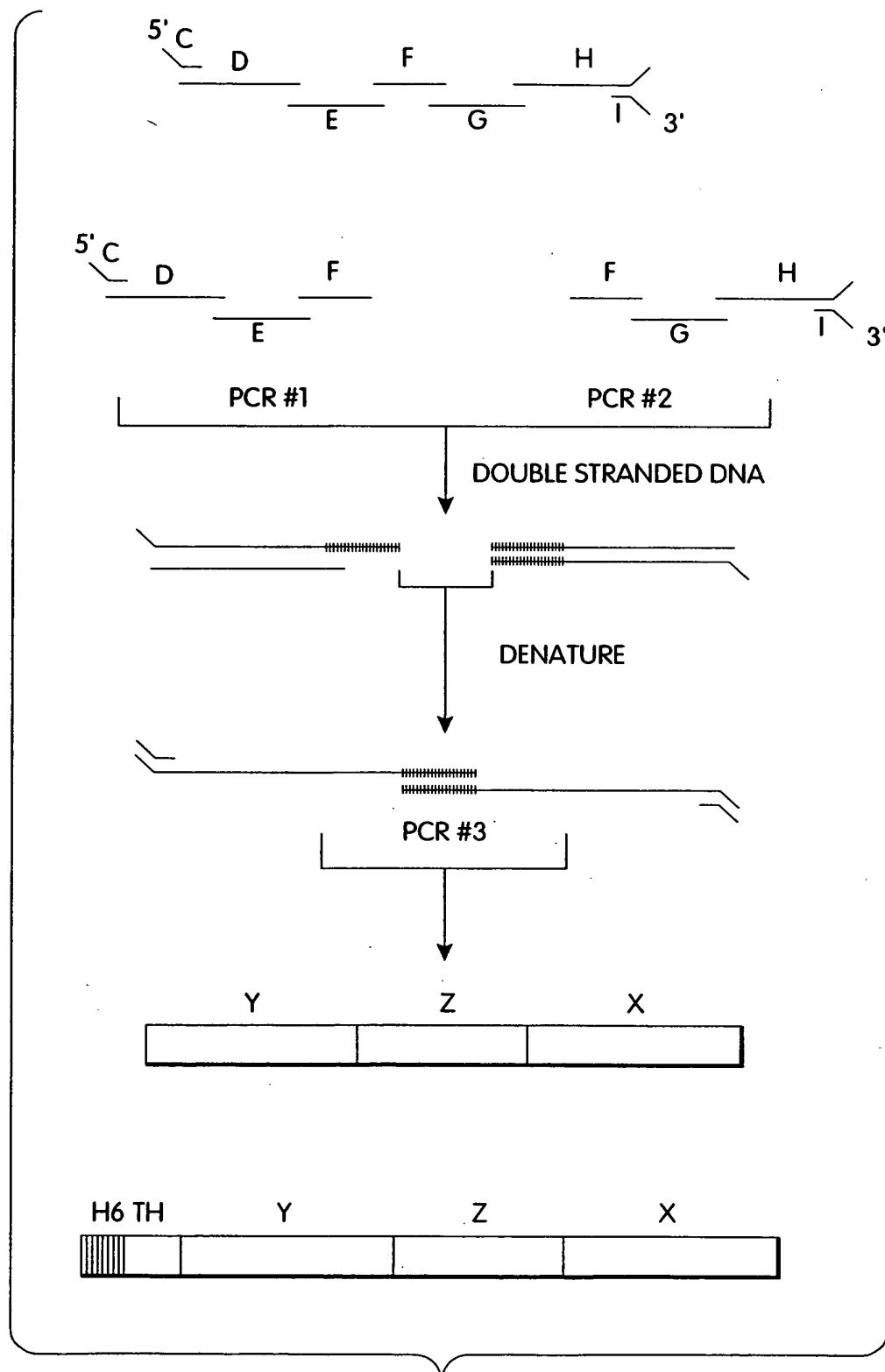


Fig. 26

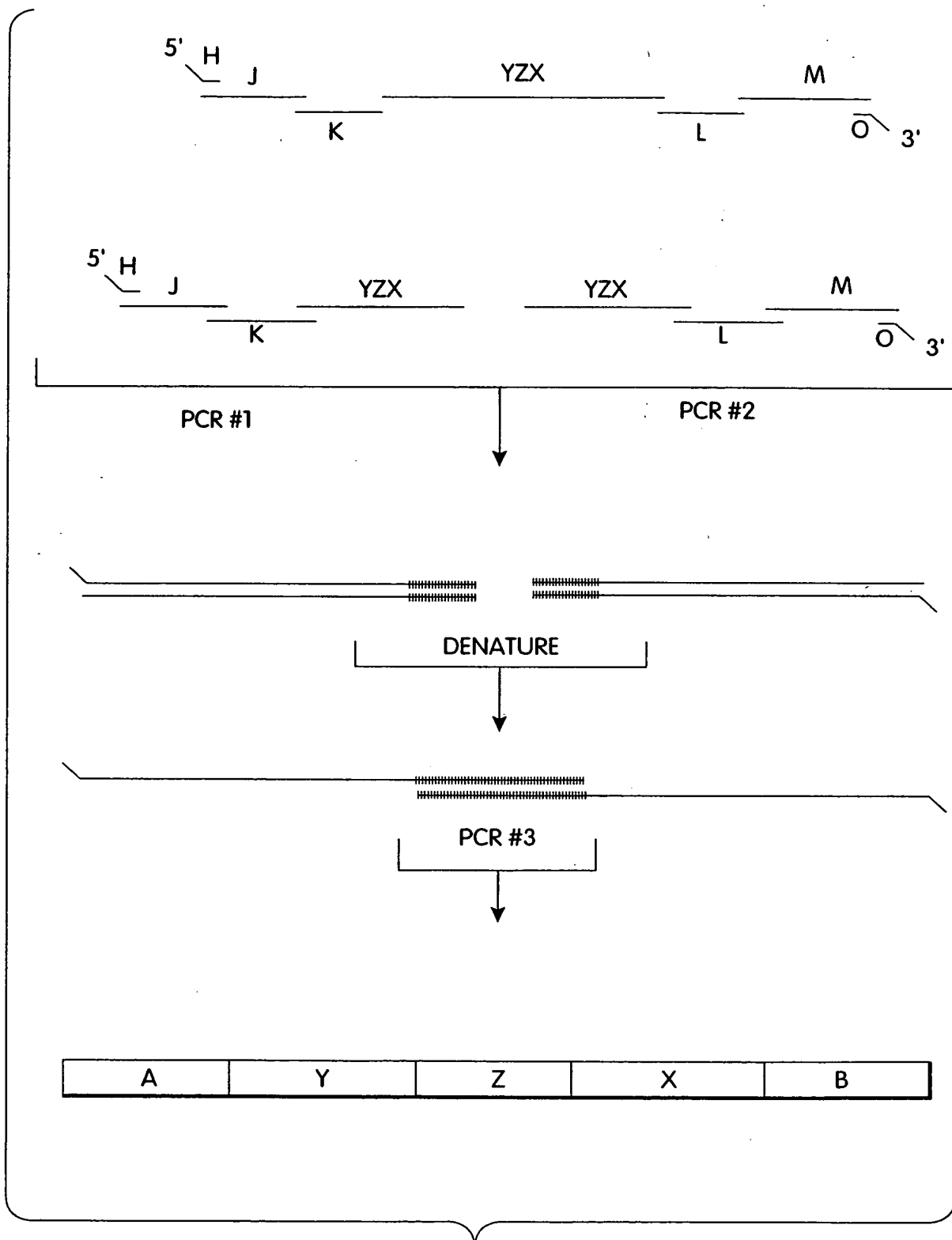


Fig. 27



C 5' BAM HI
GGGGATCCAAAGCTCTGCCGGTGT 3'
K A L P V V

D 5' BAM HI
GGGGATCCAAAGCTCTGCCGGTGTCTGTGAAACGCTCGTATCCTGAAAAAACTGCGTTGACGCTAAATGACCGAA
K A L P V V L E N A R I L K N C V D A K M T E
GAAGACAAAGAA 3'
E D K E

E 3' CTTCCTCTGTTCTTAAGAAGCGACAACGATTGCCATTGCTTGACGACGACCTGGACAGAGAC 5'
E E D K E F F A V A N G N E L L L D L S L

F 5' CTGGACCTGTCTCTGACCACCAAGTTAACGCTACCGAACCGGAACGT 3'
L D L S L T K V N A T E P E R

G 3' TGGCTTGGCCCTTGCACTTGCACTGCAACTGGACAAGGACTGGCCCATGGGGCCTG 5'
T E P E R K R D V D L F L T G T P D

H 5' ACCGGTACCCCGGACGAATACGTTGAACAGGTTGCTCAGTACAAAGCTCTGCCGGTTAGTCTAGACTGCAGAAG
T G T P D E Y V E Q V A Q Y K A L P V - - XBAl PSTI
CTTGGATCCCC 3'
HINDIII ECORI

Fig. 28A



I 3' CGAGACGGCCAAATCATCAGATCTGACGCTCTTGAACCTAGGG 5'
A L P V - - XBAI PSTI HINDIII ECORI

J 5' GGGGATCCGAAGAAGACAAAGAAAACGCTCTGTCTCTGCTG 3'
BAM HI E E D K E N A L S L L

K 3' GACAGAGACGACCTGTTTATAGATGTGGAGAGCGGACTTTCGAGACGGCCAAACAGACCTT 5'
L S L L D K I Y T S P L K A L P V L E

L 3' CGAGTCATGTTTCGAGACGGCCAAATACCCACTTCGACAAAGTCTTGTGGCAACTT 5'
A Q Y K A L P V M G E A V Q N T V E

M 5' CAGAACACCGTTGAAGACCTGAAACTGAACACCCCTGGTCTGTAATGTAACCTGCAGAATTCCCC 3'
Q N T V E D L K L N T L G R - PST I ECORI

N 5' GGGGATCCGAAGAAGACAAA 3'
BAM HI E E D K

O 3' TGAACCCCTCTACTTACATTGACGCTCTTAAGGG 5'
T L G R - PST I ECORI

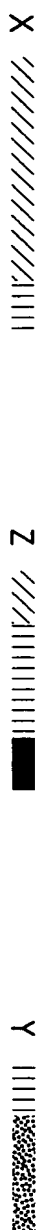
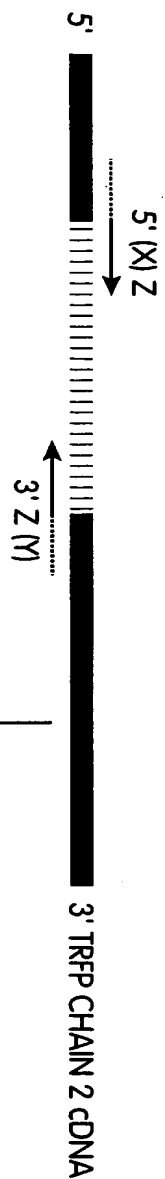
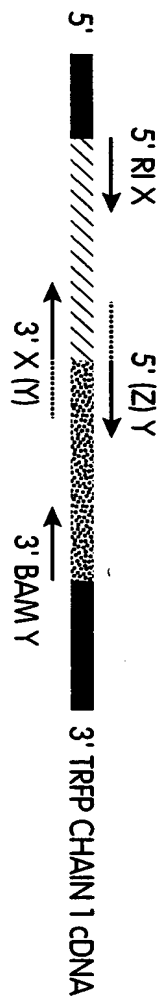
Fig. 28B



ATGGGTCACCACCACCACCACGAATTCCTGGTCCGGTGATCC
M G H H H H H H E F L V P R G S
↓
AAAGCTCTGCCGGTTGTTCTGGA¹AAACGCTCGTATCCTGAAAAACTGC
K A L P V V L E N A R I L K N C
GTTGACGCTAAATGACCGAAGAAGACAAGAATTCTCGCTGTTGCT
V D A K M T E E D K E F F A V A
AACGTAACGAAC²TGCTGTGACCTGTCTCTGACCAAGTTAACCT
N G N E L L L D L S L T K V N A
ACCGAACCGGAACGTAACGTGACGTGACCTGTCCCTGACCGGTACC
T E P E R K R D V D L F L T G T
CCGGACGAATACGTTGAACAAGGTGCTCAGTACAAGCTCTGCCGGTT
P D E Y V E Q V A Q Y K A L P V

Fig. 29

1) PCR INDIVIDUAL EPITOPES



2) LINK ISOLATED EPITOPES BY POOLING/PCR

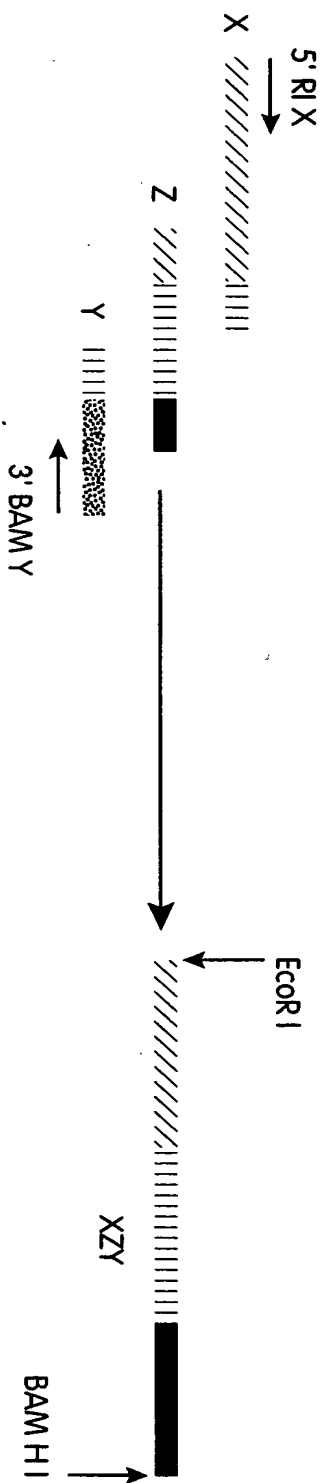


Fig. 30



5' PRIMERS

XZY CONSTRUCT

5' XRI K R D V D L
5' -GGGGAATTCAAGAGGGATGTTGACCTA-3'
 ECOR I X

 L P V | F F A V A N
5' (X) Z 5' -CTACCTGTATTTTTCGCGGTGGCCAAT-3'
 X Z

 P E R | K A L P V V
5' (Z) Y 5' -CCAGAGAGAAAGCACTACCTGTAGTA-3'
 Z Y

YXZ CONSTRUCT

5' YRI K A L P V V
5' -GGGGAATTCAAGCACTACCTGTAGTA-3'
 ECOR I Y

 D K E | K R D V D L
5' (Y) X 5' -GATAAGGAGAAAGAGGGATGTTGACCTA-3'
 Y X

 L P V | F F A V A N
5' (X) Z 5' -CTACCTGTATTTTTCGCGGTGGCCAAT-3'
 X Z

ZXY CONSTRUCT

5' ZRI F F A V A N G
5' -GGGGAATTCTTTGCGGTGGCCAATGGA-3'
 ECOR I Z

 K R D V D L P
5' (Z) X 5' -AAGAGGGATGTTGACCTATTC-3'
 X

Fig. 31A

Fig. 31 B



XZY

	X	Z	Y
<u>KRDVDL</u>			
<u>KALPV</u>	<u>FFAVAN</u>		
<u>FFAVAN</u>			
		<u>ATEPERKAL</u>	
		<u>PERKALPVV</u>	
			<u>TEEDKE</u>

YXZ

	Y	X	Z
<u>KALPVV</u>			
<u>TEEDKE</u>	<u>KRDVDL</u>		
<u>KRDVDL</u>			
		<u>KALPVFFA</u>	
		<u>LPVFFAVAN</u>	
			<u>ATEPER</u>

ZXY

	Z	X	Y
<u>FFAVANG</u>			
<u>NATEPER</u>	<u>KRDVDL</u>		
<u>KRDVDLP</u>			
		<u>QYKALPVVL</u>	
			<u>MTEEDKE</u>

Fig. 32

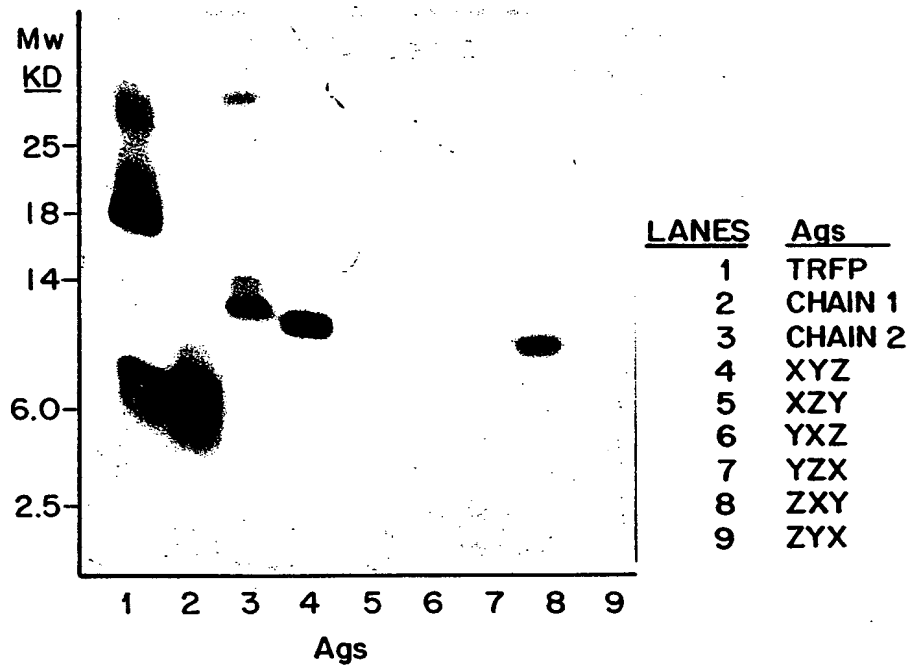


Fig. 33

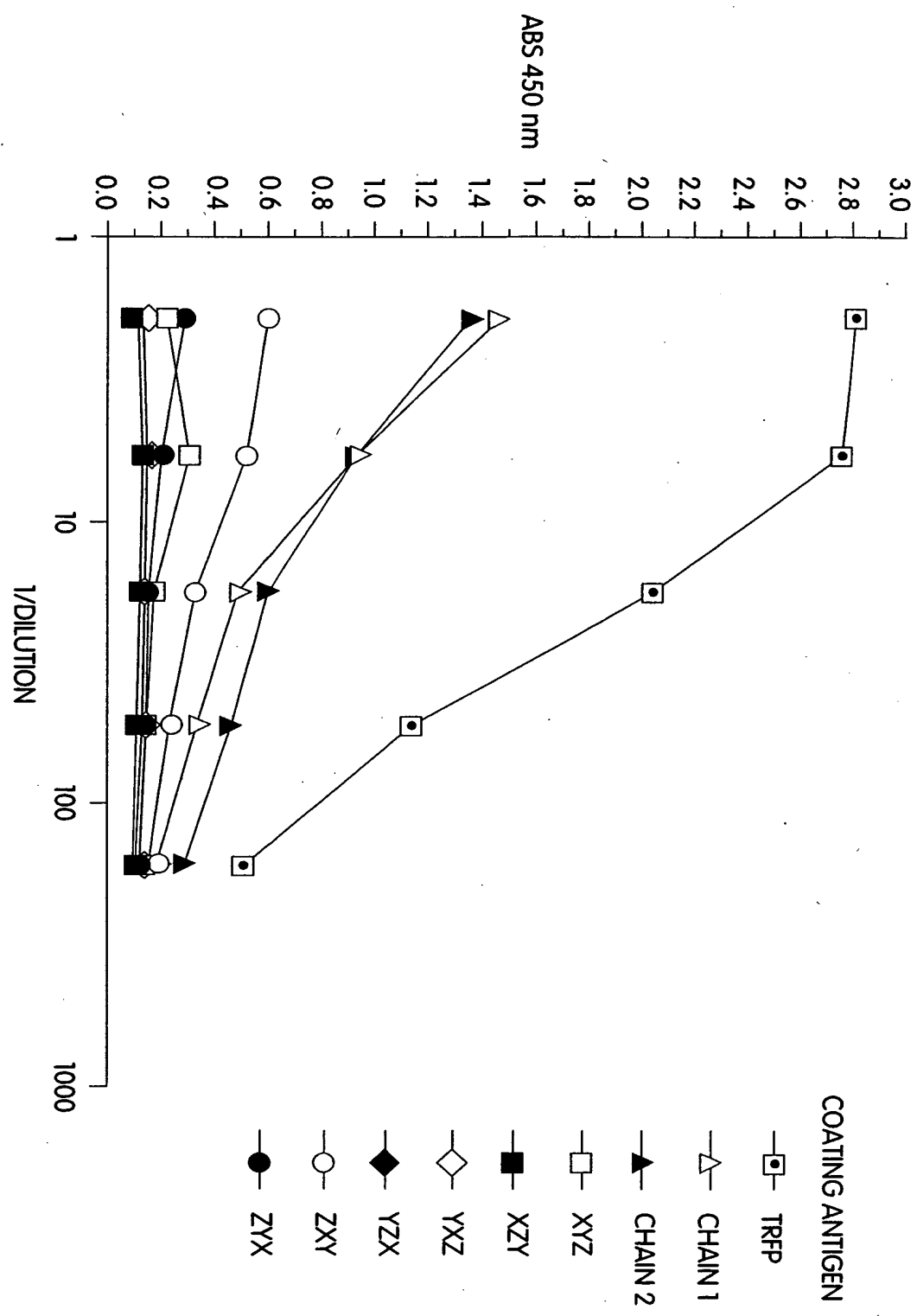


Fig. 34

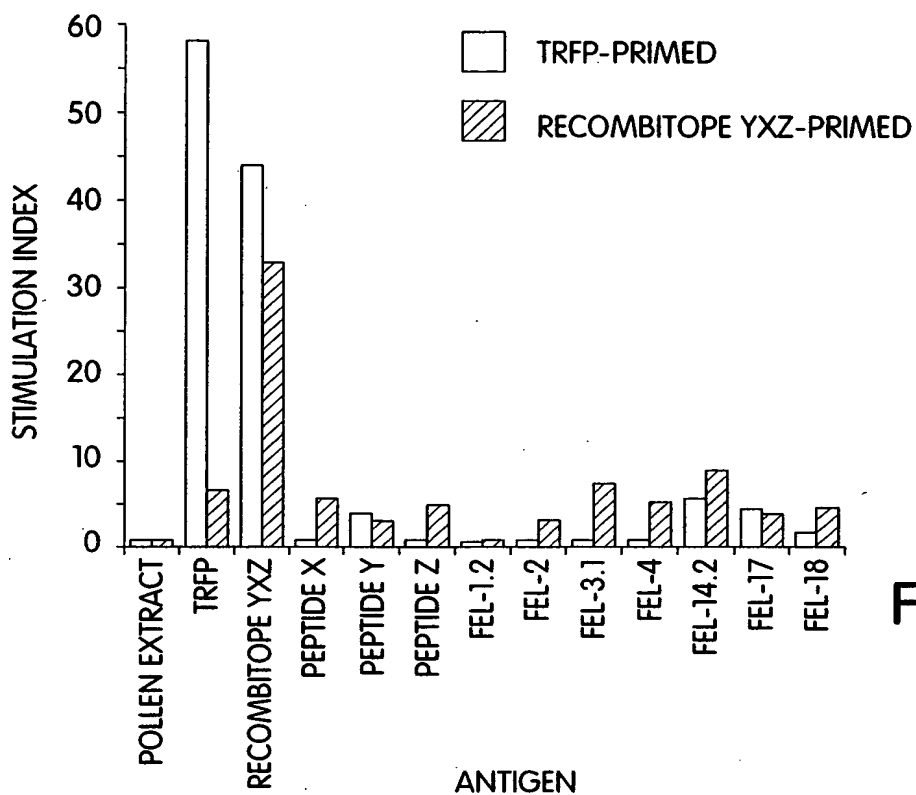


Fig. 35A

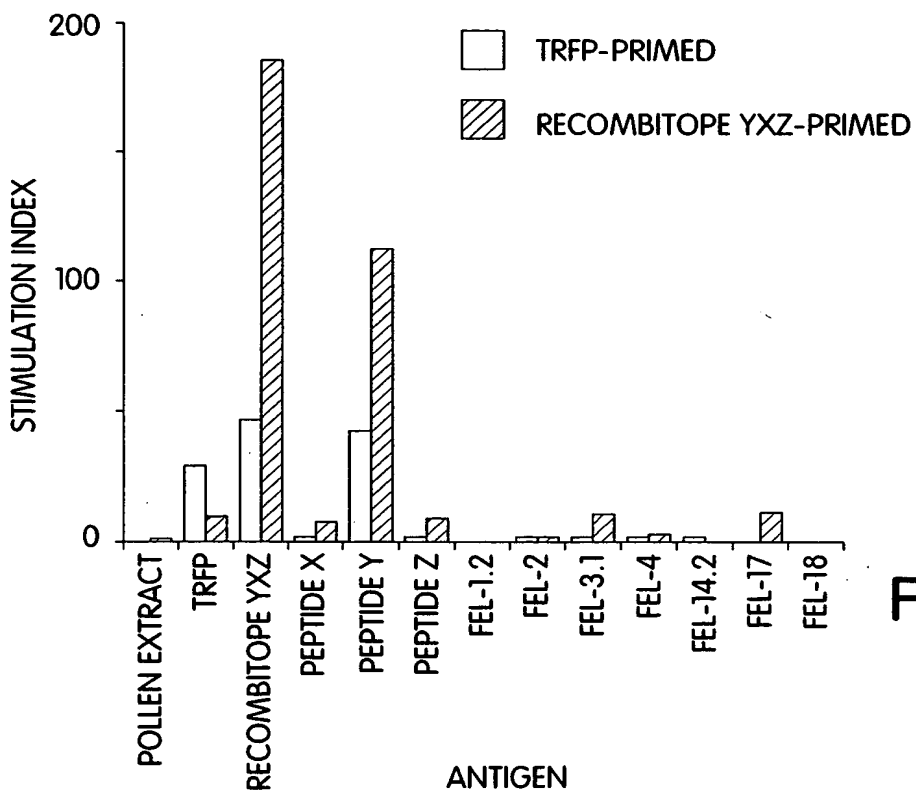


Fig. 35B

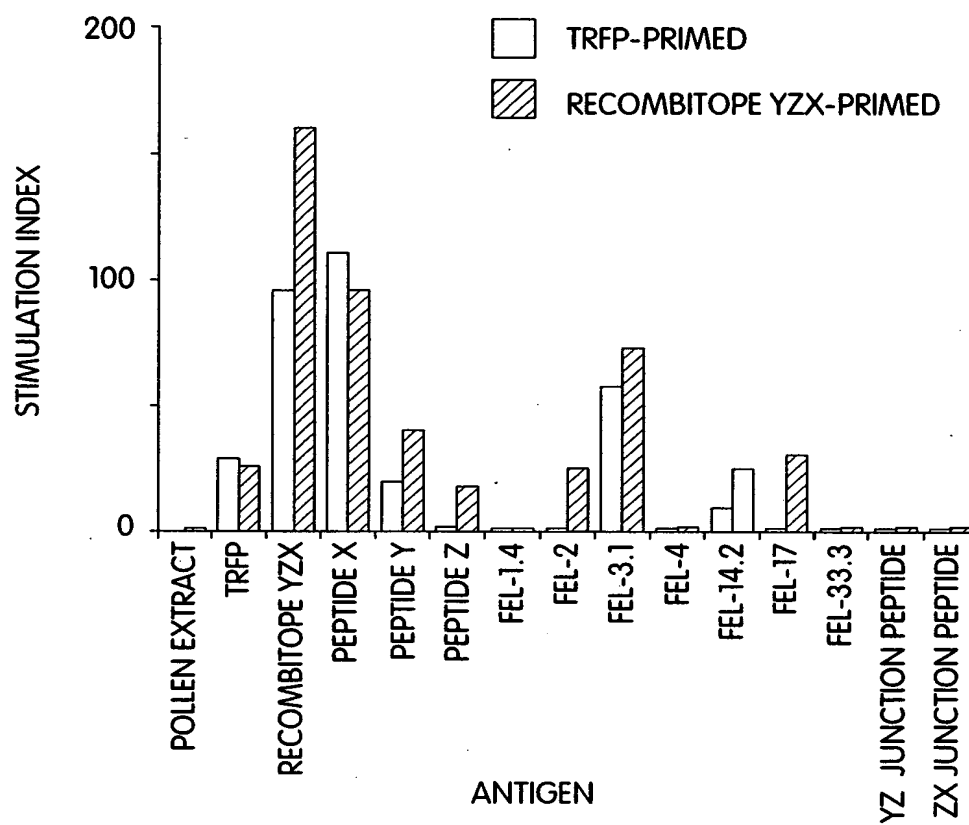


Fig. 35C

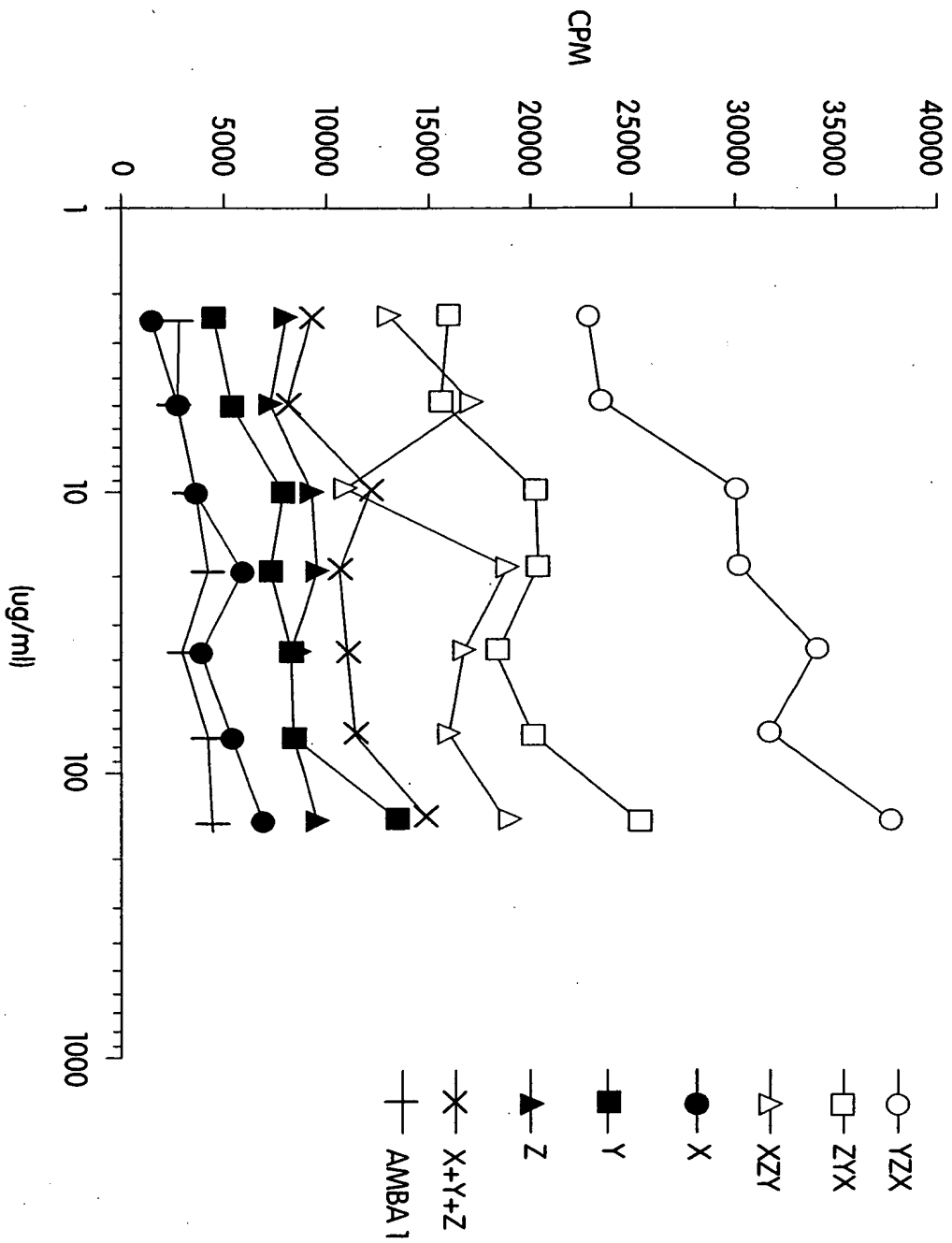


Fig. 36

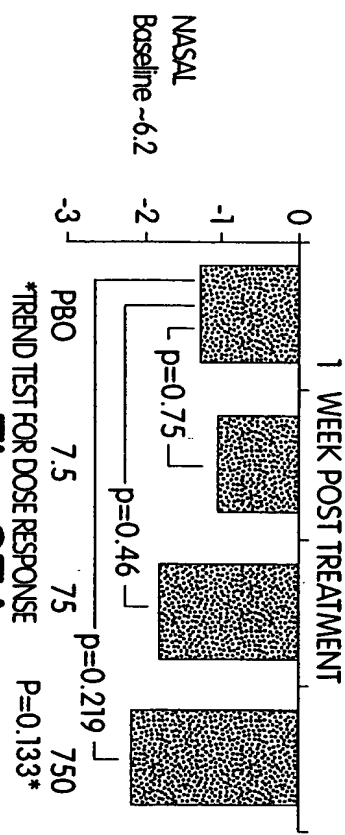
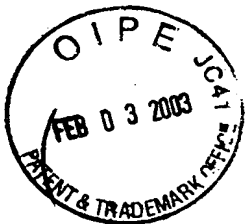


Fig. 37A

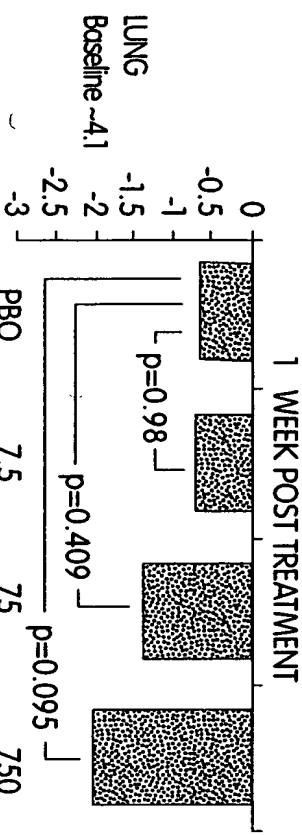


Fig. 37C

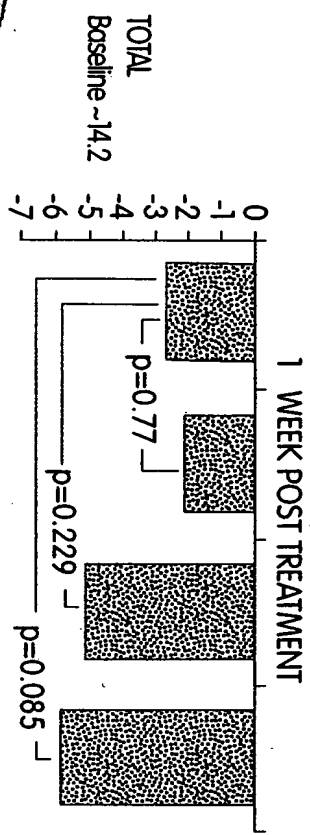


Fig. 37E

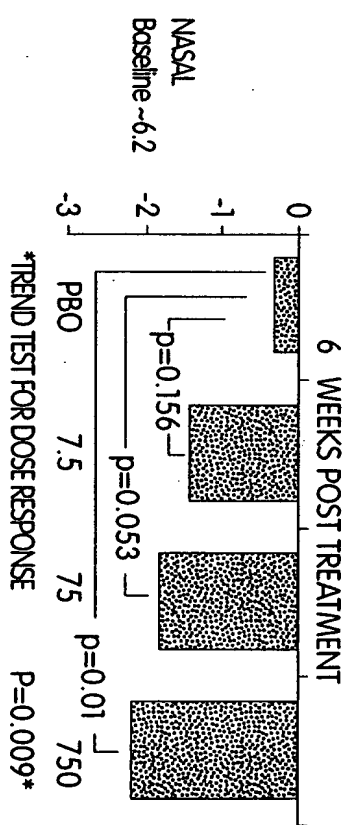


Fig. 37B

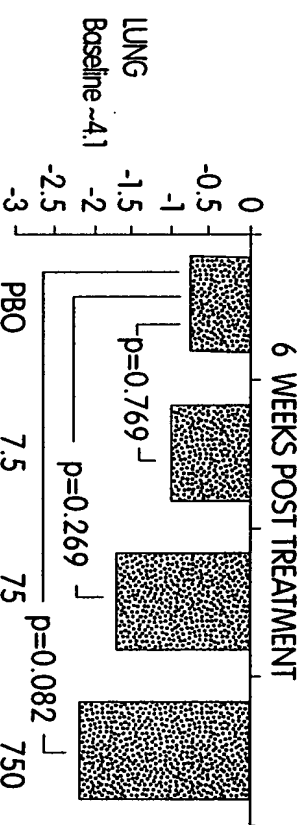


Fig. 37D

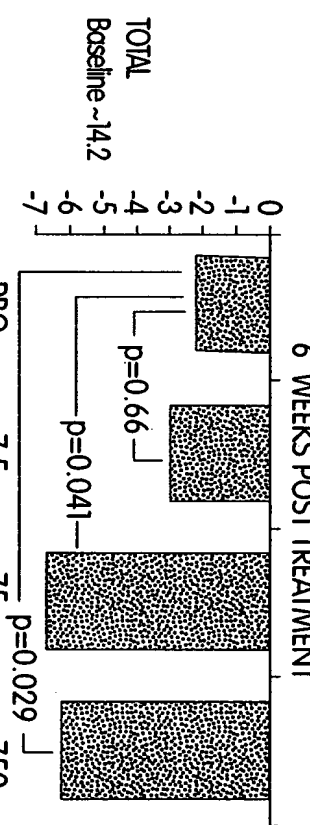


Fig. 37F